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<222> (302)..(949)

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ttatagtcta gagcgagcag gcgagatgtg aagtacctac acgcattaag tgcaaatgaa 240

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Met Thr Tyr Met Lys Lys Lys Ser Arg Asp Asp Ala Pro Val Val Ile

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gaa acc gtt caa gca gaa cat gct gaa gaa ctc acg ggc act gca gca 397

Glu Thr Val Gln Ala Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala

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45

ttc gat gct gga cag gca gac atg cca aca tgg ggc gag cta gtc gca 445

Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala

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gaa cat gca gat agc gtt tac cgc ctc gcg tac cgt ctt tcc ggc aac 493

Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn

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cag cac gat gct gaa gac ctg acc caa gaa aca ttc atg cgt gtc ttc 541

Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe

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cgc tcg ttg aag agc tac cag cca ggc acc ttt gag ggc tgg ctg cac 589

Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His

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cgc atc acc acc aac ttg ttc ctt gat atg gtt cgc cac cgc ggc aag 637
 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys
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atc cgc atg gag gcg ctg cct gaa gat tat gag cgc gtt ccg ggc aat 685
 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn
 115 120 125

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gac atc acc cca gag cag gca tac acc gaa gct aac ctt gac cca gct 733
 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala
 130 135 140

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ctg cag gca gcc ctc gat gag ttg agc cca gac ttc cgc gtg gca gtg 781
 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val
 145 150 155 160

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atc ctc tgt gat gtt gtt ggt atg agc tat gac gaa atc gca gag acc 829
 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr
 165 170 175

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ctc gga gtg aaa atg ggt acc gtg cgt tcc cgt att cac cgt gga cgc 877
 Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg
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agc cag ctt cgt gca agt ttg gaa gct gca gca atg acc agc gag gaa 925
 Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu
 195 200 205

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gtt tct ttg ttg gtt cca acc cac taaagttggt gtgttttctg acacgacaaa 979
 Val Ser Leu Leu Val Pro Thr His
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 <213> Corynebacterium glutamicum

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Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala
 35 40 45
 5 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn
 50 55 60
 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe
 65 70 75 80
 10 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His
 85 90 95
 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys
 100 105 110
 15 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn
 115 120 125
 20 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala
 130 135 140
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 25 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr
 165 170 175
 Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg
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 210 215

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 ccgcaatggt gccgtcaagg agcgcatcgg cgagcaccag cgaccgcct cgtcgaagaa 180
 gcgccagggc ggcgtcgaca agcgcttta aatccatggg ggagacttgg ccgaagacaa 240
 gctgatagct gtcgttgga aggcgactca tcacgtcgag cgggcgcgag agcaagaagc 300
 gtacgcggct gggggaatag ccggcctcgc ggaagagtgc ttggcctgg cgctgatgct 360
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 tccgctcaga gtgcaaaaac gaagaagtgt ccgcccacat ggacctcaaa gcacggcttg 180
 ccagcctcgc cactgagtgc atgcctggcc ctggcgcgaga gaatttagca atgcagcgcc 240
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<223> sigE

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30 ccgcaatggt gccgtcaagg agcgcatcgg cgagcaccag cgcaccgcct cgtcgaagaa 180

gcggccaggc ggcgtcgaca agcgcttta aatccatggg ggagacttgg ccgaagacaa 240

35 gctgatatgct gtcgttggca aggcgactca tcacgtcgag cgggcgcgag agcaagaagc 300

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ctgattcagg atcaatgcag gtcagtgtgg tggtatcggc cagtcggttc aggatataca 420

40 gaccaccaa ccgagcagcc ggggtaatcg cgatggcacc agtggagccg ttgccattgg 480

tggtggcagc caaagtgggt agcagctggc cagtcatttc atccggggcg gggagaccga 540

45 actcggcggc gtcttcacga gcgcgcgcta cagcagcgtc ggtttcagta gtggactcga 600

cataagtgcg aagatactcg aaggcggtac tcacgcgtta tagtctagag cgagcaggcg 660

agatgtgaag tacctacacg cattaagtgc aatgaattc acaattgcc aagatgcac 720

50 aggatgtaat ctgatttcc caagttcagt ggggcaaa atg act tat atg aaa aag 776

Met Thr Tyr Met Lys Lys

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 Lys Ser Arg Asp Asp Ala Pro Val Val Ile Glu Thr Val Gln Ala Glu

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15

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cat gct gaa gaa ctc acg ggc act gca gca ttc gat gct gga cag gca 872
 His Ala Glu Glu Leu Thr Gly Thr Ala Ala Phe Asp Ala Gly Gln Ala
 25 30 35

5 gac atg cca aca tgg ggc gag cta gtc gca gaa cat gca gat agc gtt 920
 Asp Met Pro Thr Trp Gly Glu Leu Val Ala Glu His Ala Asp Ser Val
 40 45 50

10 tac cgc ctc gcg tac cgt ctt tcc ggc aac cag cac gat gct gaa gac 968
 Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn Gln His Asp Ala Glu Asp
 55 60 65 70

15 ctg acc caa gaa aca ttc atg cgt gtc ttc cgc tcg ttg aag agc tac 1016
 Leu Thr Gln Glu Thr Phe Met Arg Val Phe Arg Ser Leu Lys Ser Tyr
 75 80 85

20 cag cca ggc acc ttt gag ggc tgg ctg cac cgc atc acc acc aac ttg 1064
 Gln Pro Gly Thr Phe Glu Gly Trp Leu His Arg Ile Thr Thr Asn Leu
 90 95 100

25 ttc ctt gat atg gtt cgc cac cgc ggc aag atc cgc atg gag gcg ctg 1112
 Phe Leu Asp Met Val Arg His Arg Gly Lys Ile Arg Met Glu Ala Leu
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30 cct gaa gat tat gag cgc gtt ccg ggc aat gac atc acc cca gag cag 1160
 Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn Asp Ile Thr Pro Glu Gln
 120 125 130

35 gca tac acc gaa gct aac ctt gac cca gct ctg cag gca gcc ctc gat 1208
 Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala Leu Gln Ala Ala Leu Asp
 135 140 145 150

40 gag ttg agc cca gac ttc cgc gtg gca gtg atc ctc tgt gat gtt gtt 1256
 Glu Leu Ser Pro Asp Phe Arg Val Ala Val Ile Leu Cys Asp Val Val
 155 160 165

45 ggt atg agc tat gac gaa atc gca gag acc ctc gga gtg aaa atg ggt 1304
 Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr Leu Gly Val Lys Met Gly
 170 175 180

50 acc gtg cgt tcc cgt att cac cgt gga cgc agc cag ctt cgt gca agt 1352
 Thr Val Arg Ser Arg Ile His Arg Gly Arg Ser Gln Leu Arg Ala Ser
 185 190 195

55 ttg gaa gct gca gca atg acc agc gag gaa gtt tct ttg ttg gtt cca 1400
 Leu Glu Ala Ala Ala Met Thr Ser Glu Glu Val Ser Leu Leu Val Pro
 200 205 210

acc cac taaagttggt gtgttttctg acacgacaaa cgcaaattgtc gtgtcatttt 1456
 Thr His
 215

tgcagctcag tgcattatatt tggggttcgt ggtgcggaca gggaacttat cacaggcgac 1516

55 atccgtttttg agtagtaggt atcttgata agaagttacc cacatccttg aaagtcgaga 1576

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 35 40 45
 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn
 50 55 60
 35 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe
 65 70 75 80
 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His
 85 90 95
 40 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys
 100 105 110
 45 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn
 115 120 125
 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala
 130 135 140
 50 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val
 145 150 155 160
 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr
 165 170 175
 55 Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg
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Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu
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